

GTAAACCAC ACTATTC ATG CAA AAG GGT GTA GGG TTA CTG AGG ACA GTT	50
Met Gln Lys Gly Val Gly Leu Leu Arg Thr Val	
1 5 10	
CCC TTG GTA CCT TCA GTC TCT GGT CAG ATT GAC CTT TTG GTA CTG TGT	98
Pro Leu Val Pro Ser Val Ser Gly Gln Ile Asp Leu Leu Val Leu Cys	
15 20 25	
ATG TGT ATA AAA ACG ACT ACT CCT CAT ATA TTT ATT TCT GAT TAT AAG	146
Met Cys Ile Lys Thr Thr Thr Pro His Ile Phe Ile Ser Asp Tyr Lys	
30 35 40	
ATA ATA TAT TCT GGA AAA CAC TGG AAA ATA CAT	179
Ile Ile Tyr Ser Gly Lys His Trp Lys Ile His	
45 50	

FIGURE 1

GTCTAAAACA AAATACAACA TTTCTTAAAT ACACTGTTTC CAGAAAGAGC TATTTTAAACA	60
GAAGCAACTC AAAGATATCC CTTCGACAGA AGTGGAAGTG CTGAAAAATG CTCATCTCTC	120
ACACAGACTT TTGATGGACA GGAGTTTCTA AGTATCATGC CTACCAACAA GCTGTAAA	178
ATG ATC ACC CTG AAC AAT CAA GAT CAA CCT GTC CCT TTT AAC AGC TCA Met Ile Thr Leu Asn Asn Gln Asp Gln Pro Val Pro Phe Asn Ser Ser	226
1 5 10 15	
CAT CCA GAT GAA TAC AAA ATT GCA GCC CTT GTC TTC TAT AGC TGT ATC His Pro Asp Glu Tyr Lys Ile Ala Ala Leu Val Phe Tyr Ser Cys Ile	274
20 25 30	
TTC ATA ATT GGA TTA TTT GTT AAC ATC ACT GCA TTA TGG GTT TTC AGT Phe Ile Ile Gly Leu Phe Val Asn Ile Thr Ala Leu Trp Val Phe Ser	322
35 40 45	
TGT ACC ACC AAG AAG AGA ACC ACG GTA ACC ATC TAT ATG ATG AAT GTG Cys Thr Thr Lys Lys Arg Thr Thr Val Thr Ile Tyr Met Met Asn Val	370
50 55 60	
GCA TTA GTG GAC TTG ATA TTT ATA ATG ACT TTA CCC TTT CGA ATG TTT Ala Leu Val Asp Leu Ile Phe Ile Met Thr Leu Pro Phe Arg Met Phe	418
65 70 75 80	
TAT TAT GCA AAA GAT GCA TGG CCA TTT GGA GAG TAC TTC TGC CAG ATT Tyr Tyr Ala Lys Asp Ala Trp Pro Phe Gly Glu Tyr Phe Cys Gln Ile	466
85 90 95	
ATT GGA GCT CTC ACA GTG TTT TAC CCA AGC ATT GCT TTA TGG CTT CTT Ile Gly Ala Leu Thr Val Phe Tyr Pro Ser Ile Ala Leu Trp Leu Leu	514
100 105 110	
GCC TTT ATT AGT GCT GAC AGA TAC ATG GCC ATT GTA CAG CCG AAG TAC Ala Phe Ile Ser Ala Asp Arg Tyr Met Ala Ile Val Gln Pro Lys Tyr	562
115 120 125	
GCC AAA GAA CTT AAA AAC ACG TGC AAA GCC GTG CTG GCG TGT GTG GGA Ala Lys Glu Leu Lys Asn Thr Cys Lys Ala Val Leu Ala Cys Val Gly	610
130 135 140	
GTC TGG ATA ATG ACC CTG ACC ACG ACC ACC CCT CTG CTA CTG CTC TAT Val Trp Ile Met Thr Leu Thr Thr Thr Thr Pro Leu Leu Leu Leu Tyr	658
145 150 155 160	
AAA GAC CCA GAT AAA GAC TCC ACT CCC GCC ACC TGC CTC AAG ATT TCT Lys Asp Pro Asp Lys Asp Ser Thr Pro Ala Thr Cys Leu Lys Ile Ser	706
165 170 175	

FIGURE 2A

GAC ATC ATC TAT CTA AAA GCT GTG AAC GTG CTG AAC CTC ACT CGA CTG Asp Ile Ile Tyr Leu Lys Ala Val Asn Val Leu Asn Leu Thr Arg Leu 180 185 190	754
ACA TTT TTT TTC TTG ATT CCT TTG TTC ATC ATG ATT GGG TGC TAC TTG Thr Phe Phe Phe Leu Ile Pro Leu Phe Ile Met Ile Gly Cys Tyr Leu 195 200 205	802
GTC ATT ATT CAT AAT CTC CTT CAC GGC AGG ACG TCT AAG CTG AAA CCC Val Ile Ile His Asn Leu Leu His Gly Arg Thr Ser Lys Leu Lys Pro 210 215 220	850
AAA GTC AAG GAG AAG TCC ATA AGG ATC ATC ATC ACG CTG CTG GTG CAG Lys Val Lys Glu Lys Ser Ile Arg Ile Ile Ile Thr Leu Leu Val Gln 225 230 235 240	898
GTG CTC GTC TGC TTT ATG CCC TTC CAC ATC TGT TTC GCT TTC CTG ATG Val Leu Val Cys Phe Met Pro Phe His Ile Cys Phe Ala Phe Leu Met 245 250 255	946
CTG GGA ACG GGG GAG AAC AGT TAC AAT CCC TGG GGA GCC TTT ACC ACC Leu Gly Thr Gly Glu Asn Ser Tyr Asn Pro Trp Gly Ala Phe Thr Thr 260 265 270	994
TTC CTC ATG AAC CTC AGC ACG TGT CTG GAT GTG ATT CTC TAC TAC ATC Phe Leu Met Asn Leu Ser Thr Cys Leu Asp Val Ile Leu Tyr Tyr Ile 275 280 285	1042
GTT TCA AAA CAA TTT CAG GCT CGA GTC ATT AGT GTC ATG CTA TAC CGT Val Ser Lys Gln Phe Gln Ala Arg Val Ile Ser Val Met Leu Tyr Arg 290 295 300	1090
AAT TAC CTT CGA AGC ATG CGC AGA AAA AGT TTC CGA TCT GGT AGT CTA Asn Tyr Leu Arg Ser Met Arg Arg Lys Ser Phe Arg Ser Gly Ser Leu 305 310 315 320	1138
CGG TCA CTA AGC AAT ATA AAC AGT GAA ATG TTA TGAATAATAA GGTTCCTTTCA Arg Ser Leu Ser Asn Ile Asn Ser Glu Met Leu 325 330	1191
TTTCAATCCC ATCAAAATTC ACTTCACTAA CTACTCTGGC GTCAATGGAT ATTCTGTATA	1251
ATACTATCAA GTCCCTTTTC TCTTGAAAAA ATAAATTCAT TATCTTCATT TTAAAAACTT	1311
AAA	1314

FIGURE 2B

ATTCGGCTTA CTCACTATAG GGCTCGAGCG GCGCCCGGGC AGGTCAAGAC TGCTCCTCTC	60
TGCCGACTAC AACAGATTGG AGCC ATG GCT TTG GAA CAG AAC CAG TCA ACA	111
Met Ala Leu Glu Gln Asn Gln Ser Thr	
1 5	
GAT TAT TAT TAT GAG GAA AAT GAA ATG AAC GGC ACT TAT GAC TAC AGT	159
Asp Tyr Tyr Tyr Glu Glu Asn Glu Met Asn Gly Thr Tyr Asp Tyr Ser	
10 15 20 25	
CAA TAT GAA CTG ATC TGT ATC AAA GAA GAT GTC AGA GAA TTT GCA AAA	207
Gln Tyr Glu Leu Ile Cys Ile Lys Glu Asp Val Arg Glu Phe Ala Lys	
30 35 40	
GTT TTC CTC CCT GTA TTC CTC ACA ATA GTT TTC GTC ATT GGA CTT GCA	255
Val Phe Leu Pro Val Phe Leu Thr Ile Val Phe Val Ile Gly Leu Ala	
45 50 55	
GGC AAT TCC ATG GTA GTG GCA ATT TAT GCC TAT TAC AAG AAA CAG AGA	303
Gly Asn Ser Met Val Val Ala Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg	
60 65 70	
ACC AAA ACA GAT GTG TAC ATC CTG AAT TTG GCT GTA GCA GAT TTA CTC	351
Thr Lys Thr Asp Val Tyr Ile Leu Asn Leu Ala Val Ala Asp Leu Leu	
75 80 85	
CTT CTA TTC ACT CTG CCT TTT TGG GCT GTT AAT GCA GTT CAT GGG TGG	399
Leu Leu Phe Thr Leu Pro Phe Trp Ala Val Asn Ala Val His Gly Trp	
90 95 100 105	
GTT TTA GGG AAA ATA ATG TGC AAA ATA ACT TCA GCC TTG TAC ACA CTA	447
Val Leu Gly Lys Ile Met Cys Lys Ile Thr Ser Ala Leu Tyr Thr Leu	
110 115 120	
AAC TTT GTC TCT GGA ATG CAG TTT CTG GCT TGT ATC AGC ATA GAC AGA	495
Asn Phe Val Ser Gly Met Gln Phe Leu Ala Cys Ile Ser Ile Asp Arg	
125 130 135	
TAT GTG GCA GTA ACT AAA GTC CCC AGC CAA TCA GGA GTG GGA AAA CCA	543
Tyr Val Ala Val Thr Lys Val Pro Ser Gln Ser Gly Val Gly Lys Pro	
140 145 150	
TGC TGG ATC ATC TGT TCC TGT GTC TGG ATG GCT GCC ATC TTG CTG AGC	591
Cys Trp Ile Ile Cys Ser Cys Val Trp Met Ala Ala Ile Leu Leu Ser	
155 160 165	

FIGURE 3A

ATA CCC CAG CTG GTT TTT TAT ACA GTA AAT GAC AAT GCT AGG TGC ATT	639
Ile Pro Gln Leu Val Phe Tyr Thr Val Asn Asp Asn Ala Arg Cys Ile	
170 175 180 185	
CCC ATT TTC CCC CGC TAC CTA AGA ACA TCA ATG AAA GCA TTG ATT CAA	687
Pro Ile Phe Pro Arg Tyr Leu Arg Thr Ser Met Lys Ala Leu Ile Gln	
190 195 200	
ATG CTA GAG ATC TGC ATT GGA TTT GTA GTA CCC TTT CTT ATT ATG GGG	735
Met Leu Glu Ile Cys Ile Gly Phe Val Val Pro Phe Leu Ile Met Gly	
205 210 215	
GTG TGC TAC TTT ATC ACA GCA AGG ACA CTC ATG AAG ATG CCA AAC ATT	783
Val Cys Tyr Phe Ile Thr Ala Arg Thr Leu Met Lys Met Pro Asn Ile	
220 225 230	
AAA ATA TCT CGA CCC CTA AAA GTT CTG CTC ACA GTC GTT ATA GTT TTC	831
Lys Ile Ser Arg Pro Leu Lys Val Leu Leu Thr Val Val Ile Val Phe	
235 240 245	
ATT GTC ACT CAA CTG CCT TAT AAC ATT GTC AAG TTC TGC CGA GCC ATA	879
Ile Val Thr Gln Leu Pro Tyr Asn Ile Val Lys Phe Cys Arg Ala Ile	
250 255 260 265	
GAC ATC ATC TAC TCC CTG ATC ACC AGC TGC AAC ATG AGC AAA CGC ATG	927
Asp Ile Ile Tyr Ser Leu Ile Thr Ser Cys Asn Met Ser Lys Arg Met	
270 275 280	
GAC ATC GCC ATC CAA GTC ACA GAA AGC ATC GCA CTC TTT CAC AGC TGC	975
Asp Ile Ala Ile Gln Val Thr Glu Ser Ile Ala Leu Phe His Ser Cys	
285 290 295	
CTC AAC CCA ATC CTT TAT GTT TTT ATG GGA GCA TCT TTC AAA AAC TAC	1023
Leu Asn Pro Ile Leu Tyr Val Phe Met Gly Ala Ser Phe Lys Asn Tyr	
300 305 310	
GTT ATG AAA GTG GCC AAG AAA TAT GGG TCC TGG AGA AGA CAG AGA CAA	1071
Val Met Lys Val Ala Lys Lys Tyr Gly Ser Trp Arg Arg Gln Arg Gln	
315 320 325	
AGT GTG GAG GAG TTT CCT TTT GAT TCT GAG GGT CCT ACA GAG CCA ACC	1119
Ser Val Glu Glu Phe Pro Phe Asp Ser Glu Gly Pro Thr Glu Pro Thr	
330 335 340 345	
AGT ACT TTT AGC ATT TAAAGGTAAA ACTGCTCTGC CTTTGTCTTG GATACATATG	1174
Ser Thr Phe Ser Ile	
350	
AATGATGCTT TCCCCTCAAA TAAAACATCT GCATTATTCT GAAACTCAAA TCTCAGACGC	1234
CGTGGTTGCA ACTTATAATA AAGAATGGGT TGGGGGAAGG GGGAGAAATA AAAGCCAAGA	1294
AGAAGAAACA AGATAATAAA TGTACAAAAC ATGAAAATTA AAATGAACAA TATAGGAAAA	1354

FIGURE 3B

TAATTGTAAC AGGCATAAGT GAATAAACT CTGCTGTAAC GAAGAAAAC TTGTGGTGAT 1414
AATTTGTAT CTTGGTTGCA GTGGTGCTTA TACCAATCTA CACCAGTGAT AAAATGACCC 1474
AGAACTATTT CCCCCCTTGT TCCCATTTCA ATTTCTGGT TTTGACATTA TAGTATAATT 1534
ATGTTAGATG GAACC 1549

FIGURE 3C

094065-0200
1002/20" 56907650

GATGCATGCT CGAGCGGCCG CCAGTGTGAT GGATATCTGC AGAATTCGGC TTACTCACTA	60
TAGGGCTCGA GCGGCCGCCG GGGCAGGTCC CTCCAACAAG ACGCAGCACA GAGACACCAC	120
CTACCTAACA CAGGCGACTC TGAGCACTCT CTCTCTGGGA CTGGGCAGAG CGGCAAACGG	180
TCACCTCTCA GACAGCCTTT GACAGACAGG AGGTTCTACA TACCATGGGA GCCAGCCTGC	240
TGTAAGATGG CCACCCTGAG CAATCACAAC CAGCTTGATC TTTCTAATGG CTCACACCCA	300
GAGGAATACA AAATCGCAGC CCTAGTCTTC TACAGCTGCA TCTTCCTGAT TGGGCTGTTT	360
GTTAATGTCA CTGCGTTGTG GGTTTTTCAGC TGTACGACCA AGAAAAGAAC ACAGTGACCA	420
TCTACATG ATG AAC GTT GCA CTA CTG GAC CTC GTA TTT ATA CTC AGT CTG	470
Met Asn Val Ala Leu Leu Asp Leu Val Phe Ile Leu Ser Leu	
1 5 10	
CCC TTT CGG ATG TTT TAC TAT GCA AAA GGC GAG TGG CCA TTT GGA GAG	518
Pro Phe Arg Met Phe Tyr Tyr Ala Lys Gly Glu Trp Pro Phe Gly Glu	
15 20 25 30	
TAC TTC TGC CAC ATT CTT GGG GCC CTG GTG GTG TTT TAC CCA AGC CTC	566
Tyr Phe Cys His Ile Leu Gly Ala Leu Val Val Phe Tyr Pro Ser Leu	
35 40 45	
GCT CTG TGG CTT CTT GCT TTC ATT AGT GCT GAC AGA TAC ATG GCC ATC	614
Ala Leu Trp Leu Leu Ala Phe Ile Ser Ala Asp Arg Tyr Met Ala Ile	
50 55 60	
GTA CAG CCA AAA TAT GCC AAG GAG CTG AAG AAC ACC GGC AAG GCC GTG	662
Val Gln Pro Lys Tyr Ala Lys Glu Leu Lys Asn Thr Gly Lys Ala Val	
65 70 75	
CTT GCG TGT GGG GGG GTC TGG GTA ATG ACC CTG ACC ACC ACT GTC CCC	710
Leu Ala Cys Gly Gly Val Trp Val Met Thr Leu Thr Thr Thr Val Pro	
80 85 90	
CTG CTA CTG CTC TAC GAA GAC CCA GAC AAT GCC TCC TCC CCG GCC ACC	758
Leu Leu Leu Leu Tyr Glu Asp Pro Asp Asn Ala Ser Ser Pro Ala Thr	
95 100 105 110	
TGC CTG AAG ATC TCC GAC ATC ACC CAC TTA AAA GCT GTC AAC GTG CTC	806
Cys Leu Lys Ile Ser Asp Ile Thr His Leu Lys Ala Val Asn Val Leu	
115 120 125	
AAC TTC ACG CGA CTC ATA TTT TTC TTC CTG ATC CCT TTG TTC ATC ATG	854
Asn Phe Thr Arg Leu Ile Phe Phe Phe Leu Ile Pro Leu Phe Ile Met	
130 135 140	

FIGURE 4A

ATC GGG TGC TAC GTG GTC ATC ATT CAC AGT CTC CTC CGA GGG CAG ACG	902
Ile Gly Cys Tyr Val Val Ile Ile His Ser Leu Leu Arg Gly Gln Thr	
145 150 155	
TCT AAG CTG AAG CCC AAG GTC AAG GAG AAG TCC ATA CGG ATC ATC ATG	950
Ser Lys Leu Lys Pro Lys Val Lys Glu Lys Ser Ile Arg Ile Ile Met	
160 165 170	
ACC CTC CTG CTG CAG GTG CTC GTC TGC TTC GTG CCC TTC CAC ATC TGC	998
Thr Leu Leu Leu Gln Val Leu Val Cys Phe Val Pro Phe His Ile Cys	
175 180 185 190	
TTT GCC GTC CTG ATG CTA CAA GGA CAG GAG AAC AGC TAT AGC CCC TGG	1046
Phe Ala Val Leu Met Leu Gln Gly Gln Glu Asn Ser Tyr Ser Pro Trp	
195 200 205	
GGA GCC TTC ACC ACC TTC CTC ATG AAC CTC AGC ACC TGT CTC GAT GTA	1094
Gly Ala Phe Thr Thr Phe Leu Met Asn Leu Ser Thr Cys Leu Asp Val	
210 215 220	
GTC CTC TAC TAC ATC GTT TCC AAA CAG TTC CAG GCT CGA GTC ATC AGC	1142
Val Leu Tyr Tyr Ile Val Ser Lys Gln Phe Gln Ala Arg Val Ile Ser	
225 230 235	
GTC ATG CTG TAC CGC AAT TAC CTT CGC AGT GTT CGC AGA AAA AGT GTC	1190
Val Met Leu Tyr Arg Asn Tyr Leu Arg Ser Val Arg Arg Lys Ser Val	
240 245 250	
CGA TCG GGC AGT TTA CGG TCA CTT AGC AAC ATG AAC AGT GAG ATG CTT	1238
Arg Ser Gly Ser Leu Arg Ser Leu Ser Asn Met Asn Ser Glu Met Leu	
255 260 265 270	
TGAGTCAGAG CAAGCTGCCA GTCTTCAGTC TCTTT	1273

FIGURE 4B

G CTA CAA GGA CAG GAG AAC AGC TAT AGC CCC TGG GGA GCC TTC ACC	46
Leu Gln Gly Gln Glu Asn Ser Tyr Ser Pro Trp Gly Ala Phe Thr	
1 5 10 15	
ACC TTC CTC ATG AAC CTC AGC ACC TGT CTC GAT GTA GTC CTC TAC TAC	94
Thr Phe Leu Met Asn Leu Ser Thr Cys Leu Asp Val Val Leu Tyr Tyr	
20 25 30	
ATC GTT TCC AAA CAG TTC CAG GCT CGA GTC ATC AGC GTC ATG CTG TAC	142
Ile Val Ser Lys Gln Phe Gln Ala Arg Val Ile Ser Val Met Leu Tyr	
35 40 45	
CGC AAT TAC CTT CGC AGT GTT CGC AGA AAA AGT GTC CGA TCG GGC AGT	190
Arg Asn Tyr Leu Arg Ser Val Arg Arg Lys Ser Val Arg Ser Gly Ser	
50 55 60	
TTA CGG TCA CTT AGC AAC ATG AAC AGT GAG ATG CTT TGAGTCAGAG	236
Leu Arg Ser Leu Ser Asn Met Asn Ser Glu Met Leu	
65 70 75	
CAAGCTGCCA GTCTTCAGTC TCTTTAAAAT TCTTTTCCTA TCTACTTTTCG GGTGAACCAG	296
CATTCTACAC TATCCAGTCC CTTCTCTAAC AAAGAGAAAT AATAATGATG AACTTTAAAA	356
ACTTCTGCGG TATTCTGTGT ATTCTAGCCA CATGATTAAA AACT	400

FIGURE 5

091065-0704

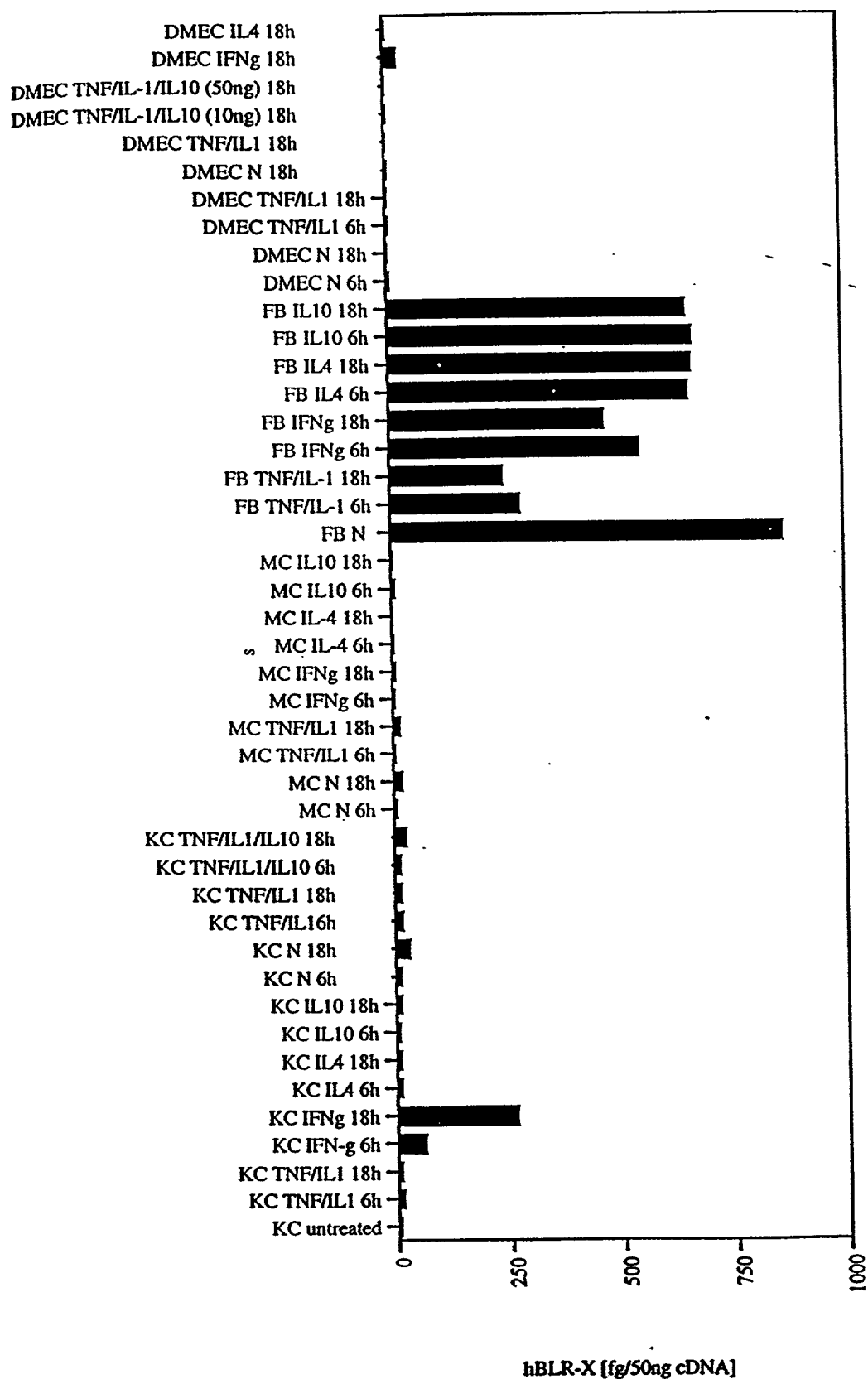


Fig. 6

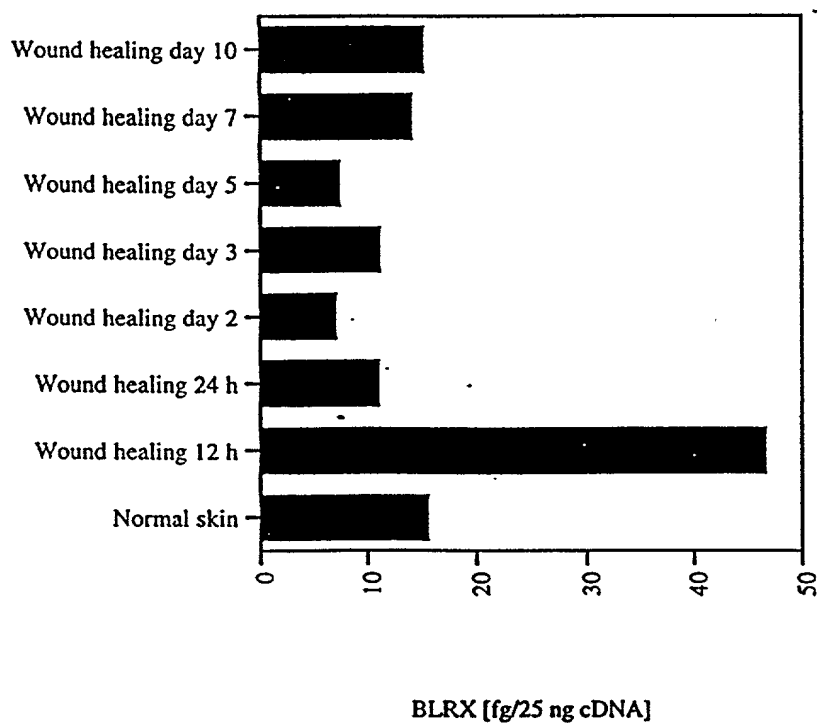


Fig. 7